

Result	Query
No.	Score Match Length DB ID Description

states/sec

190

ed,

```

LINE      51147122
RES
source
Location/Qualifiers
1..87
/organism="Dictyostellium discoideum"
/strain="AA-3"
/db_xref="taxon:44589"
<!--87
CDS

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/codon_start=1
/product="protein kinase 4"
/protein_id="AA033189.1"
/db_xref="GI:167724"
/translation="NLIDQYGHKILDFGFAKRTENKSMC"
BASE COUNT      36 a   12 c   14 g   25 t
ORIGIN

Query Match      0.6%   Score 29.6; DB 3; Length 87;
Best Local Similarity 59.5%; Pred. NO. 1.8e+04;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4051 aaatctcttaccctcctggattcaaacctggagagatttgcatttcagtaag 4110
Db 1 NATCTTATATGATCAATATGACATATTAACTCAGATGTTTGGATTGCAANAAGA 60

QY 4111 ctcaaaacaatgccagaccatg 4134
Db 61 ATCAGAGAAATACCAAAAGATG 84

RESULT 2
AR007403/c
LOCUS      AR007403      100 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5750497.
ACCESSION AR007403
VERSION   AR007403.1 GI:3966887
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 100)
AUTHORS   Havelund,S., Halst.o slashed.m.J., Jonassen,I., Andersen,A.Sloth.
and Markussen,J.
TITLE     Acylated insulin
JOURNAL   Patent: US 5750497-A 4 12-MAY-1998;
FEATURES  Location/Qualifiers
            source
            1..100
            /organism="unknown"
BASE COUNT 29 a   22 c   23 g   26 t
ORIGIN

Query Match      0.5%   Score 26; DB 6; Length 100;
Best Local Similarity 55.6%; Pred. NO. 1.7e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 aagaatgaagctagtagaatgacttggaattcttcaactactactgtatgtaa 4528
Db 97 AAGCTGACGACGCTAAGGCTATCGTTGAACAATGTTGTACTTCTATCTGTTTGTAC 38

QY 4529 tattacataaagactgtcgaagacag 4558
Db 37 CAATTGGAAAACACTGCTGCTAGACGAC 8

RESULT 3
AF025984
LOCUS      AF025984      96 bp      DNA      linear      VRT 30-OCT-1997
DEFINITION Paralicthys dentatus lactate dehydrogenase (LDHA) gene, allele
            pLDHA2, Intron 6.
ACCESSION AF025984
VERSION   AF025984.1 GI:2570847
KEYWORDS  summer flounder.
SOURCE    Paralicthys dentatus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
            Pleuronectoidae; Paralicthyidae; Paralicthys.
REFERENCE 1 (bases 1 to 96)
AUTHORS   Quattro,J.M. and Jones,W.J.

Amplification Primers That Target Locus-Specific Introns in
Actinopterygian Fishes
Unpublished
Quattro,J.M. and Jones,W.J.
Direct Submission
Submitted (22-SEP-1997) Biological Sciences, University of South
Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
Location/Qualifiers
            source
            1..96
            /organism="Paralicthys dentatus"
            /db_xref="taxon:66718"
            1..96
            /gene="LDHA"
            /note="lactate dehydrogenase gene"
            /allele="pLDHA2"
            1..96
            /gene="LDHA"
            /number=6
BASE COUNT      24 a   22 c   20 g   30 t
ORIGIN

Query Match      0.5%   Score 25.4; DB 5; Length 96;
Best Local Similarity 64.4%; Pred. NO. 2.4e+05;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 4423 gccagcagctcctcgcaccattcgtttgtcaagggttgcacagatgaagaagcct 4481
Db 14 GTGGACAAATCTTAGAGATTTCATTACAAACAGTGTGCACATGACTAATGATCCT 72

RESULT 4
AX033167
LOCUS      AX033167      70 bp      DNA      linear      BCT 21-SEP-2000
DEFINITION Sequence 3 from Patent WO0045176.
ACCESSION AX033167
VERSION   AX033167.1 GI:10280029
KEYWORDS  Escherichia coli.
SOURCE    Escherichia coli.
ORGANISM  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE 1 (bases 1 to 70)
AUTHORS   Gallusser,A., Karl,J., Lill,H., Stahl,P., Krueger,K. and Borgya,A.
TITLE     Method of identifying n-terminal probop
JOURNAL   Patent: WO 0045176-A 03-AUG-2000;
            GALLUSSER ANDREAS (DE); KARL JOHANN (DE); LILL HELMUT (DE);
            STAHL PETER (DE); KRUEGER KERSTIN (DE); BORGYA ANNELESE (DE);
            ROCHE DIAGNOSTICS GMBH (DE)
FEATURES  Location/Qualifiers
            source
            1..70
            /organism="Escherichia coli"
            /db_xref="taxon:562"
BASE COUNT      10 a   19 c   21 g   20 t
ORIGIN

Query Match      0.5%   Score 25.2; DB 1; Length 70;
Best Local Similarity 62.3%; Pred. NO. 2.7e+05;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1778 agggcgctgctgctgaagacatctaccaggttcacgtgcaggaggttctcgaggact 1837
Db 8 AGCAGGCTGTTCACCTGACCTGTCGACAGTTTACCCTGCGAGGTGGTGTCTTCC 67

QY 1838 tg 1839
Db 68 TG 69

RESULT 5
AX033159

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Best Local Similarity 63.3%. Pred. No. 3.5e+05;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 45 taccctccccccagcacacctccacagcgtgaacgcgtgtcaacccaacatcagagaa 104
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 TTCATCTCCACCCACACACCACCGCAGTAGTAAAAAAGTAAAGAAAAACTTAGGATTAA 21

RESULT 9
ARI40801/c
LOCUS ARI40801
DEFINITION Sequence 78 from patent US 5207816.
ACCESSION ARI40801
VERSION ARI40801.1 GI:14483297
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 71)
AUTHORS Gold, L., Janjic, N. and Pogratis, N.
TITLE High affinity oligonucleotide ligands to growth factors
JOURNAL Patent: US 5207816-A 78 27-MAR-2001;
FEATURES
    Location/Qualifiers
        1..71
            /organism="unknown"
BASE COUNT 15 a 16 c 22 g 18 t
ORIGIN

```

```

RESULT 30
193480/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORIGIN
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

193480
Sequence 78 from patent US 5731144.
193480
193480.1 GI:3937950
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 71)
Toothman,P.J., Ringquist,S. and Gold,L.
High affinity TGF.beta. nucleic acid ligands
Patent: US 5731144-A 78 24-MAR-1998;
Location/Qualifiers
1..71
/organism="unknown"
15 a 16 c 22 g 18 t

Query Match 0.5% Score 24.6; DB 6; Length 71;
Best Local Similarity 65.5% Pred. No. 3.9e+05;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 3958 gacatcgtgattagctgtgtattccaagcagatcacccattgcgatcaagtcctcc 4012
|||||
Db 56 GAAGCGCTAAGTAAAGTAGTATTAAAAACATACACCCCGCTGGCGGCATCGCTCGCC 2
|||||

```

RESULT 11  
195107/c  
LOCUS 195107 DNA 71 bp linear PAT 01-DEC-1998  
DEFINITION Sequence 78 from patent US 5731424.  
ACCESSION 195107

```

195107.1 GI:3939577
Unknown.
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 71)
AUTHORS Toothman,P.J., Ringquist,S. and Gold,L.
TITLE High affinity TGF-beta2 nucleic acid ligands and inhibitors
JOURNAL Patent: US 5731424-A 78 24-MAR-1998;
FEATURES Location/Qualifiers
source 1..71
BASE COUNT 15 a 16 c 22 g 18 t
ORIGIN

Query Match 0.5% Score 24.6; DB 6; Length 71;
Best Local Similarity 65.5% Pred.No.3.9e+05;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 3958 gaacatgtagtgctgtattcaaacgaagcaccattgcgatcacagtccctc 4012
||||| || | ||||| ||| || | || | || ||||| |||
Db 56 GAAGACGTAAGTAGTATTAAACAATACCCTCCCTGCCGCATCGTCCTCC 2

RESULT 12
LOCUS S76509/c S76509
DEFINITION DLS8 (A) [hypervariable minisatellite MS32] human, individual
MACH Genomic, 73 nt].
S76509
S76509.1 GI:243382
human individual MACH.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 73)
AUTHORS Monckton,D.G. and Jeffreys,A.J.
TITLE Minisatellite 'isoallele' discrimination in pseudohomozygotes by
single molecule PCR and variant repeat mapping
JOURNAL Genomics 11 (2), 465-467 (1991)
MEDLINE 92120671
REMARK GenBank staff at the National Library of Medicine created this
entry (NCBI gi243382.1) from the original journal article.
This sequence comes from Figure 2.
FEATURES Source 1..73
Location/Qualifiers
Source /organism="Homo sapiens"
gene /db_xref="taxon:9606"
1..73
/gene="DLS8"
/allele="A"
BASE COUNT 41 a 0 c 0 g 32 t
ORIGIN

Query Match 0.5% Score 24.4; DB 9; Length 73;
Best Local Similarity 60.6% Pred.No.4.5e+05;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy 4914 tgtaatgcaaaggcgattactgaattaaagaagaagttcttitttcataaatgg 4973
||||| || | ||||| ||| || | ||||| ||| ||||| ||| |||
Db 72 TATTATAATAAATAATTAAATTTAAATTAATTTTTTTTAAATTAATTTAT 13

Oy 4974 ttattt 4979
|||||
Db 12 TTATT 7

RESULT 13
LOCUS DROTANSIN/c DROTANSIN
DEFINITION DROTANSIN (A) [hypervariable minisatellite MS32] human, individual
MACH Genomic, 73 nt].
S76509
S76509.1 GI:243382
human individual MACH.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 73)
AUTHORS Monckton,D.G. and Jeffreys,A.J.
TITLE Minisatellite 'isoallele' discrimination in pseudohomozygotes by
single molecule PCR and variant repeat mapping
JOURNAL Genomics 11 (2), 465-467 (1991)
MEDLINE 92120671
REMARK GenBank staff at the National Library of Medicine created this
entry (NCBI gi243382.1) from the original journal article.
This sequence comes from Figure 2.
FEATURES Source 1..73
Location/Qualifiers
Source /organism="Homo sapiens"
gene /db_xref="taxon:9606"
1..73
/gene="DLS8"
/allele="A"
BASE COUNT 41 a 0 c 0 g 32 t
ORIGIN

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 10:21:32 : Search time 487.5 Seconds  
(without alignments)  
17574.160 Million cell updates/sec

Title: US-09-676-436-3  
Perfect score: 4990  
Sequence: 1 ctgaagacttccatga.....ggcttatattgaagatc 4990  
Scoring table: IDENTITY.NUC  
Gapop.10.0, Gapexl.1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 2046006

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :		N_Geneseq_032802 :	
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2:	/SIDSI/gcgdata/geneseq-emb1/NA1981.DAT :	2:	/SIDSI/gcgdata/geneseq-emb1/NA1981.DAT :
3:	/SIDSI/gcgdata/geneseq-emb1/NA1982.DAT :	3:	/SIDSI/gcgdata/geneseq-emb1/NA1982.DAT :
4:	/SIDSI/gcgdata/geneseq-emb1/NA1983.DAT :	4:	/SIDSI/gcgdata/geneseq-emb1/NA1983.DAT :
5:	/SIDSI/gcgdata/geneseq-emb1/NA1984.DAT :	5:	/SIDSI/gcgdata/geneseq-emb1/NA1984.DAT :
6:	/SIDSI/gcgdata/geneseq-emb1/NA1985.DAT :	6:	/SIDSI/gcgdata/geneseq-emb1/NA1985.DAT :
7:	/SIDSI/gcgdata/geneseq-emb1/NA1986.DAT :	7:	/SIDSI/gcgdata/geneseq-emb1/NA1986.DAT :
8:	/SIDSI/gcgdata/geneseq-emb1/NA1987.DAT :	8:	/SIDSI/gcgdata/geneseq-emb1/NA1987.DAT :
9:	/SIDSI/gcgdata/geneseq-emb1/NA1988.DAT :	9:	/SIDSI/gcgdata/geneseq-emb1/NA1988.DAT :
10:	/SIDSI/gcgdata/geneseq-emb1/NA1989.DAT :	10:	/SIDSI/gcgdata/geneseq-emb1/NA1989.DAT :
11:	/SIDSI/gcgdata/geneseq-emb1/NA1990.DAT :	11:	/SIDSI/gcgdata/geneseq-emb1/NA1990.DAT :
12:	/SIDSI/gcgdata/geneseq-emb1/NA1991.DAT :	12:	/SIDSI/gcgdata/geneseq-emb1/NA1991.DAT :
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15:	/SIDSI/gcgdata/geneseq-emb1/NA1994.DAT :	15:	/SIDSI/gcgdata/geneseq-emb1/NA1994.DAT :
16:	/SIDSI/gcgdata/geneseq-emb1/NA1995.DAT :	16:	/SIDSI/gcgdata/geneseq-emb1/NA1995.DAT :
17:	/SIDSI/gcgdata/geneseq-emb1/NA1996.DAT :	17:	/SIDSI/gcgdata/geneseq-emb1/NA1996.DAT :
18:	/SIDSI/gcgdata/geneseq-emb1/NA1997.DAT :	18:	/SIDSI/gcgdata/geneseq-emb1/NA1997.DAT :
19:	/SIDSI/gcgdata/geneseq-emb1/NA1998.DAT :	19:	/SIDSI/gcgdata/geneseq-emb1/NA1998.DAT :
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24:	/SIDSI/gcgdata/geneseq-emb1/NA2003.DAT :	24:	/SIDSI/gcgdata/geneseq-emb1/NA2003.DAT :

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.2	0.5	78	AAT50934	Mouse p53-recognit
2	26.6	0.5	92	AA19445	Human secreted pro
3	25.6	0.5	100	AA08600	Human insulin deri
4	25.2	0.5	70	AA17899	Human G-protein su
5	25.2	0.5	70	AA17899	Human brain natriu
6	25.2	0.5	89	AA17899	Human brain natriu
7	25.2	0.5	99	AA17899	Human brain natriu
8	25.2	0.5	99	AA17899	Human brain natriu
9	25.2	0.5	54	AA17346	Primer 307-3195 fo

C 10	25	0.5	91	22	ABA69691	Human foetal liver
C 11	24.8	0.5	77	21	AA13392	Human secreted pro
C 12	24.8	0.5	92	22	AA06930	Reverse PCR primer
C 13	24.8	0.5	94	21	AA11499	Human secreted pro
C 14	24.8	0.5	94	21	AA11541	Human secreted pro
C 15	24.6	0.5	71	18	AA165208	Transforming grow
C 16	24.6	0.5	72	21	AA152344	CDNA encoding grol
C 17	24.6	0.5	98	20	AA123469	Human neutrophil c
C 18	24.6	0.5	82	20	AA125128	801E Bundle peptid
C 19	24.4	0.5	99	22	ABA58615	Human foetal liver
C 20	24.4	0.5	100	25	AA096411	Human insulin deri
C 21	24.4	0.5	80	22	AA172601	Human foetal liver
C 22	24.2	0.5	80	22	AA172601	Human foetal liver
C 23	24.2	0.5	80	22	AA172601	Human foetal liver
C 24	24.2	0.5	80	22	AA172601	Human foetal liver
C 25	24.2	0.5	84	21	AA123226	Human brain expres
C 26	24.2	0.5	84	21	AA123226	Human brain expres
C 27	24.2	0.5	84	21	AA123226	Human brain expres
C 28	24.2	0.5	84	21	AA123226	Human brain expres
C 29	24.2	0.5	84	21	AA123226	Human brain expres
C 30	24.2	0.5	84	21	AA123226	Human brain expres
C 31	24.2	0.5	84	21	AA123226	Human brain expres
C 32	24.2	0.5	84	21	AA123226	Human brain expres
C 33	24.2	0.5	84	21	AA123226	Human brain expres
C 34	24.2	0.5	84	21	AA123226	Human brain expres
C 35	24.2	0.5	84	21	AA123226	Human brain expres
C 36	24.2	0.5	84	21	AA123226	Human brain expres
C 37	24.2	0.5	84	21	AA123226	Human brain expres
C 38	24.2	0.5	84	21	AA123226	Human brain expres
C 39	24.2	0.5	84	21	AA123226	Human brain expres
C 40	24.2	0.5	84	21	AA123226	Human brain expres
C 41	24.2	0.5	84	21	AA123226	Human brain expres
C 42	24.2	0.5	84	21	AA123226	Human brain expres
C 43	24.2	0.5	84	21	AA123226	Human brain expres
C 44	24.2	0.5	84	21	AA123226	Human brain expres
C 45	24.2	0.5	84	21	AA123226	Human brain expres

ALIGNMENTS

RESULT	1
AA150934	
ID	AA150934 standard: cDNA: 78 BP.
AC	AA150934:
DT	07-APR-1997 (first entry)
DE	Mouse p53-recognit clone 1 5' sequence.
XX	p53 binding protein: Mdmx, tumour suppressor; cancer; ss.
XX	Mus sp.
PN	MO9641875-A1.
XX	27-DEC-1996.
PF	13-JUN-1996: 96MO-NL00239.
PR	13-JUN-1995: 95EP-0201565.
PA	(INTR-) INTROGENE BV.
PI	(UYLE-) RIJKSUNIV LEIDEN.
XX	Jochimsen A. Snavits A. Van Der Eb AJ.
XX	WPI: 1997-063462/06.
XX	Nucleic acid encoding p53-binding protein - which has homology to
XX	mouse Mdm2, for use in cancer research



OY 4529 tatttaccataaagctgtctgtggaagcag 4558  
 DB 37 CAATTGGAAACTACTGTCTTAGACCGAG 8

RESULT 4  
 ID AAH48689 standard: DNA; 60 BP.  
 AC AAH48689;  
 XX  
 XX  
 DT 19-OCT-2001 (first entry)  
 XX  
 DE Human G-protein subunit Gbeta3 Intron 9 DNA fragment #2.  
 KW Human: G-protein subunit Gbeta3; variant: high blood pressure; asthma;  
 KW hypertension; cardiac infarction; coronary disease; heart disease;  
 KW circulation disease; diabetes; psychiatric disease; Crohn's disease;  
 KW immunological disease; psoriasis; colitis ulcerosa;  
 KW transplant rejection; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE10030945-A1.  
 XX  
 XX 09-AUG-2001.  
 XX  
 XX 24-JUN-2000; 2000DE-1030945.  
 XX  
 PR 03-FEB-2000; 2000DE-1004581.  
 PR 21-FEB-2000; 2000DE-1007587.  
 XX  
 XX (SIFFT) SIFERT W.  
 PA  
 XX Sifert W;  
 PI  
 XX  
 DR WPI: 2001-490007/54.  
 XX  
 XX Use of sequence variants of the beta3 subunit of human G protein to  
 PT predict, detect, and determine drug targets for diseases including  
 PT heart, immunological and psychiatric diseases.  
 XX  
 PS Disclosure: Page 3; 14pp; German.  
 CC This invention describes a novel use for sequence variants of the human  
 CC G-protein beta3 subunit to predict physiological and pathological  
 CC pathways in the human body. The invention may be used to detect, detect  
 CC predisposition for, give a prognosis of, or treat a variety of diseases  
 CC including high blood pressure, hypertension, cardiac infarction, coronary  
 CC disease and other heart or circulation diseases, diabetes, psychiatric  
 CC diseases, immunological diseases, asthma, psoriasis, Crohn's disease,  
 CC colitis ulcerosa, transplant rejection, Crohn's disease, hepatitis B, C. This  
 CC sequence represents a segment of the human G-protein beta3 subunit  
 CC intron 9 which is used to illustrate the method of the invention.  
 XX  
 XX Sequence 60 BP: 6 A; 11 C; 6 G; 37 T; 0 other;

Query Match 0.5%; Score 25.2; DB 22; Length 60;  
 Best Local Similarity 66.7%; Pred. No. 3.4e+03;  
 Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 507 ctctgctcctcaaaagaaacgcggagcgaagaggaagaaatcgtctg 560  
 DB 58 CTCTGCTCTCAAAAAGAAAAAAGAAAAAAGACAGTACAAAGGCGTAG 5

RESULT 5  
 ID AAH1594  
 XX  
 XX AAH1594 standard: DNA; 70 BP.  
 AC AAH1594;  
 XX  
 XX

DT 21-DEC-2000 (first entry)  
 XX  
 DE Human brain natriuretic peptide N-terminal primer Pro2hum.  
 KW Brain natriuretic peptide; BNP; primer; human; detection; epitope;  
 KW heart; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02000045176-A2  
 XX  
 XX 03-AUG-2000.  
 XX  
 XX 27-JAN-2000; 2000WO-SP00602.  
 XX  
 XX 29-JAN-1999; 99DE-1003489.  
 PR 12-MAR-1999; 99DE-1011044.  
 XX  
 XX (HOFF) ROCHE DIAGNOSTICS GmbH.  
 PA  
 XX Karl J. Hill H. Stahl P. Krueger K. Borzys A. Gallusser A.  
 PI  
 XX WPI: 2000-499359/44.  
 XX  
 XX Identification of N-terminal pro-brain natriuretic peptide (pro-BNP)  
 PT using two antibodies that recognize different epitopes of the  
 PT N-terminal pro-BNP, useful for diagnosis of heart insufficiency -  
 XX  
 XX Example 1; Page 32; 35pp; German.  
 XX  
 CC This invention describes a novel method to detect N-terminal pro-brain  
 CC natriuretic peptide (BNP) in a sample using two antibodies that  
 CC recognize different epitopes of the N-terminal pro-BNP. The method can  
 CC be used for diagnosing heart insufficiency. The recombinant N-terminal  
 CC pro-BNP is useful as a standard in a method to detect N-terminal pro-BNP.  
 CC and also for production of antibodies against N-terminal pro-BNP.  
 CC This sequence represents a primer used in the cloning of recombinant  
 CC N-terminal proBNP which is described in the method of the invention.  
 XX  
 XX Sequence 70 BP: 10 A; 19 C; 21 G; 20 T; 0 other;

Query Match 0.5%; Score 25.2; DB 21; Length 70;  
 Best Local Similarity 62.9%; Pred. No. 3.7e+03;  
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 1778 agggcgctctactgagcagcagctaccagctcagtcgaggggtcttgaggagct 1837  
 DB 8 agggagctctgttccacctcagctcagtcgagcagcttaccctcgagtggtacgtgtcc 67

OY 1838 tg 1839  
 DB 68 tg 69

RESULT 6  
 ID AAT22086  
 XX  
 XX AAT22086 standard: cDNA to mRNA; 89 BP.  
 AC AAT22086;  
 XX  
 XX 02-AUG-1996 (first entry)  
 XX  
 XX Human gene signature HUNG503631.  
 XX  
 XX Gene signature: messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W05514772-A1.  
 XX



PD 01-JUN-1995.  
 XX  
 PF 11-NOV-1994; 94MO-JP01916.  
 XX  
 PR 12-NOV-1993; 93JP-0355504.  
 XX  
 PA (MATS/) MATSUBARA K.  
 PA (OKUB/) OKUBO K.  
 XX  
 PI Matsubara K., Okubo K.  
 XX  
 DR WPI: 1995-206931/27.  
 XX  
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 XX  
 PS Claim 1: Page 1039; 2245pp; Japanese.  
 XX  
 CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in AA719001-T26837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 XX  
 SQ Sequence 89 BP; 39 A; 8 C; 15 G; 27 T; 0 other;

Query Match 0.5%; Score 25.2; DB 16; Length 89;  
 Best Local Similarity 62.94; Pred. No. 4.4e+03;  
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 QY 4485 agaataatgactggaaattcttcttaactactactgtagtaattattacataaagact 4544  
 DB 13 acataaagtctatgagagaatatattataatagtagtactgtcttaataaagact 72  
 QY 4545 gt 4546  
 DB 73 gt 74

RESULT 7  
 AA792244  
 ID AA792244 standard; DNA; 99 BP.  
 XX  
 AC AA792244;  
 XX  
 DT 19-JAN-1998 (first entry)  
 XX  
 DE Mercuric ion reductase merA PCR mutagenesis primer 307-339S.  
 XX  
 KW Metal ion resistance; mercuric ion reductase; merA; mercury;  
 KW toxic heavy metal; transgenic plant; mutagenic; bacterial;  
 KW transposon; Tn21; PCR; ss.  
 XX  
 OS Synthetic.  
 OS Transposon Tn21.  
 XX  
 PI US5668294-A.  
 XX  
 PN 16-SEP-1997.  
 XX

PF 21-APR-1995; 95US-0427097.  
 XX  
 PR 21-APR-1995; 95US-0427097.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX  
 PI Meagher RB, Summers AO;  
 XX  
 DR WPI: 1997-470112/43.  
 XX  
 PT DNA encoding mercuric ion reductase in plant-expressible form - for  
 PT producing transgenic plants resistant to toxic heavy metals  
 XX  
 PS Example 1; Column 43-44; 52pp; English.  
 XX  
 CC The present sequence represents a PCR mutagenesis primer used to  
 CC mutagenise the merA coding sequence derived from transposon Tn21 to  
 CC adapt it for plant expressibility. The nucleic acid molecule produced  
 CC is useful for producing transgenic plants that are resistant to toxic  
 CC heavy metals (especially mercury) and so can be used to remediate and/or  
 CC revegetate contaminated areas. The bacterial merA gene is derived from  
 CC the transposon Tn21, which was originally isolated from the  
 CC incompatibility Group IncFII resistance plasmid NR1.  
 XX  
 SQ Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;  
 Query Match 0.5%; Score 25.2; DB 18; Length 99;  
 Best Local Similarity 54.3%; Pred. No. 4.7e+03;  
 Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
 QY 3026 atctctgactaaatgtgagatgtgaggtacaaagaccagtggtggtcctcaaggat 3085  
 DB 2 aaagaccagctatggtgagatgtgaggtacaaagaccagtggtggtcctcaaggat 51  
 QY 3086 ttgattttctcaagcaattgaacctgctttat 3119  
 DB 62 gtgagcactacaaagcaagccagctgcttat 95  
 RESULT 8  
 AAZ28594  
 ID AAZ28594 standard; DNA; 99 BP.  
 XX  
 AC AAZ28594;  
 XX  
 DT 24-DEC-1999 (first entry)  
 XX  
 DE Primer 307-339S for Tn21 merA gene.  
 XX  
 KW Organometal; resistance; transcription; translation; regulation; merA;  
 KW transposon; Tn21; merB; mercuric ion reductase; organomercury lyase; ss;  
 KW transgenic plant; detoxification; metal compound; soil; sediment; primer;  
 KW aquatic environment; bioremediation; contamination; PCR; amplification.  
 XX  
 OS Synthetic.  
 OS Transposon Tn21.  
 XX  
 PN US5965796-A.  
 XX  
 PD 12-OCT-1999.  
 XX  
 PF 19-JUN-1997; 97US-0878957.  
 XX  
 PR 21-APR-1995; 95US-0427097.  
 XX  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX  
 PI Rugh CL, Meagher RB, Summers AO;  
 XX  
 DR WPI: 1999-579950/49.  
 XX  
 PT Metal resistance sequences for producing transgenic plants -







```

RESULT 15
AAT65208/c
ID AAT65208 standard; DNA: 71 BP.
XX
XX AC AAT65208:
XX
XX DT 10-SEP-1997 (first entry)
XX
XX DE Transforming growth factor beta-1 binding ligand D 11.
XX
XX KW Transforming growth factor: beta-1; TGF-beta-1; binding ligand;
XX KW Identification; SELEX; anti-mitogenic; inhibition; cell;
XX KW Systematic Evolution of Ligands by Exponential enrichment;
XX KW epithelial; proliferation; diagnosis; treatment; fibroids;
XX KW kidney; lung; liver; dermal scarring; restenosis; ss.
XX
XX OS Synthetic.
XX
XX PN W09618579-Al.
XX
XX PD 05-DEC-1996.
XX
XX PF 30-MAY-1996; 96WO-US08014.
XX
XX PR 20-MAR-1996; 96US-0618693.
XX PR 02-JUN-1995; 95US-0458423.
XX PR 02-JUN-1995; 95US-0458424.
XX PR 05-JUN-1995; 95US-0465591.
XX PR 05-JUN-1995; 95US-0465594.
XX PR 07-JUN-1995; 95US-0479725.
XX PR 07-JUN-1995; 95US-0479783.
XX
XX PA (NEXS-) NEXSTAR PHARM INC.
XX
XX PI Gold L, Janjic N, Pagnatilis N, Ringquist S, Toothman PJ.
XX
XX DR WPI; 1997-034387/03.
XX
XX PT Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF
XX PT using SELEX, used in the diagnosis and treatment of proliferative
XX PT disorders
XX
XX PS Claim 15; Page 123; 209pp; English.
XX
XX CC The present sequence, a transforming growth factor beta-1
XX CC (TGF-beta-1) binding ligand, was identified by Systematic Evolution
XX CC of Ligands by Exponential enrichment (SELEX). Briefly a candidate
XX CC mixture of nucleic acids was contacted with TGF-beta-1, and nucleic
XX CC acids having an increased affinity to TGF-beta-1 partitioned from
XX CC the remainder of the mixture. The partitioned nucleic acids were
XX CC then amplified to yield a mixture of nucleic acids enriched for
XX CC sequences with higher affinity and specificity for binding to
XX CC TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit
XX CC epithelial cell proliferation, or in the diagnosis and treatment of
XX CC TGF-beta-1 mediated pathological conditions, e.g. fibrotic
XX CC conditions such as fibroids of the kidney, lung and liver and more
XX CC acute conditions such as dermal scarring and restenosis.
XX
XX SQ Sequence 71 BP; 15 A; 16 C; 22 G; 18 T; 0 other;

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Query Match 0.58; Score 24.6; DB 18; Length 71;
Best Local Similarity 65.5%; Pred. No. 5.7e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy 1958 gaacatgtgattagctgtattcaagcagatcacccattgcgatacagctctcc 4012
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GAAGACGTAAGTAGTAGTATTAAACATACCCCCCTCGCCGCGATCGCTCTCC 2

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Search completed: May 29, 2002, 13:05:25  
Job time: 9833 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:13:38 : Search time 3518.59 Seconds  
(without alignments)  
19141.135 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990

Sequence: 1 ctgaagacttcctgatga.....ggttattttgaaagctc 4990

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

- 1: em\_estb.\*
- 2: em\_estc.\*
- 3: em\_estd.\*
- 4: em\_este.\*
- 5: em\_estf.\*
- 6: em\_estg.\*
- 7: em\_esth.\*
- 8: em\_esti.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_hic.\*
- 12: gb\_gsa.\*
- 13: em\_gss\_hum.\*
- 14: em\_gss\_inv.\*
- 15: em\_gss\_pln.\*
- 16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	29	0.6	70	AA990067	.....
3	28.5	0.6	71	AA990067	.....
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5	27.8	0.6	83	AA990067	.....
6	27.8	0.6	94	AA990067	.....
7	27.8	0.6	100	AA990067	.....
8	27.4	0.5	91	AA990067	.....
9	27.4	0.5	98	AA990067	.....
10	26.8	0.5	100	AA990067	.....
11	26.6	0.5	81	AA990067	.....
12	26.6	0.5	82	AA990067	.....
13	26.4	0.5	87	AA990067	.....
14	26.4	0.5	95	AA990067	.....
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16	26.2	0.5	78	AA990067	.....
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19	26	0.5	98	1C	BH12076	BH12076 50384887
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21	26	0.5	98	1C	BH12076	BH12076 50384887
22	26	0.5	98	1C	BH12076	BH12076 50384887
23	26	0.5	98	1C	BH12076	BH12076 50384887
24	26	0.5	98	1C	BH12076	BH12076 50384887
25	26	0.5	98	1C	BH12076	BH12076 50384887
26	26	0.5	98	1C	BH12076	BH12076 50384887
27	26	0.5	98	1C	BH12076	BH12076 50384887
28	26	0.5	98	1C	BH12076	BH12076 50384887
29	26	0.5	98	1C	BH12076	BH12076 50384887
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31	26	0.5	98	1C	BH12076	BH12076 50384887
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33	26	0.5	98	1C	BH12076	BH12076 50384887
34	26	0.5	98	1C	BH12076	BH12076 50384887
35	26	0.5	98	1C	BH12076	BH12076 50384887
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## ALIGNMENTS

RESULT 1  
AA990067  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA990067  
Jat8f02.r1 Soares\_thymus\_2NBMT  
IMAGE:1361691.5  
55 bp  
mRNA  
linear  
EST 02-JUN-1998  
Mus musculus CDNA clone  
EST  
house mouse  
Mus musculus

REFERENCE  
AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Norris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.

TITLE  
JOURNAL

COMMENT

The WashU-HMNI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
7444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1810  
Fax: 314 286 1810

EMAIL: mmarra@wustl.edu  
This clone is available royalty-free through IMAGE Consortium (info@imgc.llnl.gov) for further information.

IMAGE Consortium (info@imgc.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 82

Location/Qualifiers

1..55

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:1361691"

/sex="male"

/clone\_lib="Soares\_thymus\_2NBMT"



[illegible]











Email: M-SaberePRCU.EUN.EG  
Seq primer: sk.

Location/Qualifiers  
1. .95

/organism="Schistosoma mansoni"

/strain="Egyptian"

/db\_xref="taxon:6183"

/clone="SMTBADAH50038SK"

/clone.lib="S. mansoni cDNA"

/lab\_host="E. coli XL Blue1"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from adult couples of S. mansoni.

cDNA was constructed and cloned simultaneously using

vector priming with the pBluescript II SK+ vector. cDNA

was directionally synthesized from the EcoRI site in the

vector to the XhoI site.

31 a 15 c 10 g 39 t

BASE COUNT  
ORIGIN

Query Match 0.5%; Score 26.4; DB 10; Length 95;  
Best Local Similarity 59.2%; Pred. No. 7.3e+04;  
Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 641 acctcttttatacagccgctcagccatcccgatattattatgaatccctactt 700

Db 5 ACTATGATTATTATACACTAGTTCAGCAATCCCTTATCTATAAAATGTTATCTTTATT 64

Qy 701 tcaagtcgactatg 716

Db 65 TGAATTTTACCATAG 80

Search completed: May 29, 2002, 11:17:02  
Job time: 7404 sec

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C 2	26	0.5	100	3	US-08-975-365-4
C 3	25.2	0.5	99	1	US-08-427-097-5
C 4	25.2	0.5	99	2	US-08-427-097-5
C 5	24.6	0.5	71	1	US-08-878-357-5
C 6	24.6	0.5	71	1	US-08-438-127A-78
C 7	24.6	0.5	71	1	US-08-438-127A-78
C 8	24.6	0.5	71	1	US-08-973-124-78
C 9	24.6	0.5	71	5	PCT-US98-08014-78
C 10	24.6	0.5	72	3	US-09-100-664A-5
C 11	24.4	0.5	100	1	US-08-400-256-9
C 12	24.4	0.5	100	3	US-08-975-365-9
C 13	24	0.5	97	1	US-08-182-175A-54
C 14	24	0.5	97	1	US-08-474-633A-63
C 15	23.8	0.5	97	5	PCT-US90-06412-54
C 16	23.8	0.5	83	1	US-08-672-158A-8
C 17	23.6	0.5	87	2	US-08-631-751A-4
C 18	23.4	0.5	77	1	US-07-679-052A-8
C 19	23	0.5	60	3	US-08-643-704A-37
C 20	22.8	0.5	94	4	US-09-344-888A-8
C 21	22.8	0.5	76	1	US-08-246-583-9
C 22	22.6	0.5	96	3	US-08-484-322-5
C 23	22.6	0.5	77	1	US-07-679-052A-10
C 24	22.4	0.5	90	1	US-08-123-702-21
C 25	22.4	0.4	95	2	US-08-333-176A-41
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Best Local Similarity 55.6%  Pred. NO. 6.1e+02;
Matches 50;  Conservative 0;  Mismatches 40;  Indels 0;  Gaps 0;
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Accession	Sequence	Position
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Qy	4529 tatttacaataaagctgtctgtagaagcag	4558
Db	37 CAATTGGAAACTACTGTGCTTTAGACGCAG	8

RESULT 2  
US-08-975-365-4/C  
: Sequence 4, Application US/08975365  
: Patent No. 6011007  
: GENERAL INFORMATION:  
: APPLICANT: Havelund, Svend  
: APPLICANT: Halstrom, John  
: APPLICANT: Jonassen, Ib  
: APPLICANT: Andersen, Asger Sloth  
: APPLICANT: Markussen, Jan  
: TITLE OF INVENTION: ACYLATED INSULIN  
: NUMBER OF SEQUENCES: 49  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: No. 6011007o No. 6011007th America, Inc.  
: STREET: 405 Lexington Avenue, 64th Floor  
: CITY: New York

	Query Match	0.5%	Score 26;	DB 3;	Length 100;
	Best Local Similarity	55.6%;	Pred. No. 6.1e-02;		
	Matches 50;	Conservative	Mismatches 40;	Indels	0. Caps
Qy	4469	aggaatgaagcctagtgaatatgactctggaataattctttaactactctatgatgaa	4528		
Db	97	AAGCTGACGACGCTAAGGATCTCGTTGAACAAATTGTACTTCTATCTGTTCTTGTAC	38		
Qy	4529	tatttacaataagactgtctgagaagcag	4558		
Db	37	CAATTGGAAAACTACTGTGCTTAGACGCAG	8		

RESULT 3  
US-08-427-097-5  
: Sequence 5, Application US/08427097  
: Patent No. 568294

GENERAL INFORMATION:  
APPLICANT: Neagher, Richard B.  
APPLICANT: Sommers, Anne O.  
TITLE OF INVENTION: Metal Resistance Sequences and  
TITLE OF INVENTION: Transgenic Plants  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US

```

Query Match      0.59: Score 25.2: DB 1: Length 99:
Best Local Similarity 54.3%: Pred. No. 1e-03:
Matches 51: Conservative 43: Mismatches 43: Indels 0: Gaps 0:

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      y      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      b 2 AAGACCACGCTATAGTGTGAAGCTGTTACTGCTGCATTTCGCATTCGATCGGAAGCGCATTCGAATGC 61

3086 ttgattttctacaagaacttgaaacctgcctttt 3119 .
      y      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      b 62 GTGAGCATCTACTCAAGCAAGCCAGTGTGCCTATAT 95

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RESULT 4  
US-08-878-957-5  
: Sequence 5, Application US/08878957  
: Patent No. 5965796  
: GENERAL INFORMATION:  
: APPLICANT: Meagher, Richard B.  
: APPLICANT: Summers, Anne O.  
: APPLICANT: Rugh, Clayton L.  
: TITLE OF INVENTION: Metal Resistance Sequences and  
: TITLE OF INVENTION: Transgenic Plants  
: NUMBER OF SEQUENCES: 34  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
: STREET: 5370 Manhattan Circle, Suite 201  
: CITY: Boulder  
: STATE: Colorado  
: COUNTRY: US  
: ZIP: 80303





GENERAL INFORMATION:  
APPLICANT: LARRY GOLD; NEBOJSA JANJIC; STEVEN RINQQUIST;  
APPLICANT: PAGRAITS; PENELOPE J. TOTHMAN  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH  
TITLE OF INVENTION: FACTOR (TGF  $\beta$ , PLATELET-DERIVED  
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN  
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR (hKGF)  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIORITY DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,693  
FILING DATE: 20-MARCH-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PCT-US96-08014-78

Query Match 0.5%; Score 24.6; DB 5; Length 71;  
Best Local Similarity 65.3%; Pred. No. 1.2e+03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0:  
Oy 3958 caacatgattgagctattatcaaacgaatcaccatgcagatcagatccac 4012  
Db 56 GAAGCGTAGTANGTATGATTAACATACCCCTCGCCGCGATCGCTCC 2

RESULT 9  
US-09-100-664A-5  
Sequence 5, Application US/09100664A  
Patent No. 6057129  
GENERAL INFORMATION:  
APPLICANT: YOUNG, MICHAEL W.  
APPLICANT: KLOSS, BRIAN  
APPLICANT: BLAU, JUSTIN  
APPLICANT: PRICE, JEFFREY  
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/100,664A  
FILING DATE: 19-JUN-1998  
CLASSIFICATION: A15  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-221

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-487-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 72 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-09-100-664A-5

Query Match 0.5%; Score 24.6; DB 3; Length 72;  
Best Local Similarity 59.2%; Pred. No. 1.3e+03;  
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0:  
Oy 3694 attgagagagccgatggagaggtgtacaccgcatcagcgcacacggggagctg 3753  
Db 1 ATAGATCGGATCGTTCGGCGACATCTACTGGCCACCGCATCAACACTGCCGAGGAG 60  
Oy 3754 atggccatgaa 3764  
Db 61 GTGGCCATCAA 71

RESULT 10  
US-08-400-256-9/c  
Sequence 9, Application US/08400256  
Patent No. 5750497  
GENERAL INFORMATION:  
APPLICANT: Havelund, Svend  
APPLICANT: Halstrom, John  
APPLICANT: Jonassen, Inger  
APPLICANT: Andersen, Asger Sloth  
APPLICANT: Mathiasen, Jon  
TITLE OF INVENTION: ACYLATED INSULIN  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5750497 of No. 5750497 disk of No. 5750497 of America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,256  
FILING DATE: 03-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Landilis, Elias J.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 1985, 220-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-9655  
TELEFAX: 212-867-0123  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-400-256-9



RESULT 13  
US-08-474-633A-63  
Sequence 63, Application US/08474633A  
Patent No. 577691  
GENERAL INFORMATION:  
APPLICANT: COMPANY: DU PONT DE NEMOURS AND  
APPLICANT: COMPANY: CHIMERIC GENES AND  
TITLE OF INVENTION: METHODS FOR INCREASING  
TITLE OF INVENTION: INCREASING THE LYSINE  
TITLE OF INVENTION: AND THREONINE CONTENT  
TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
ADDRESS: AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08474633A  
FILING DATE: 07/24/92  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DHS alpha  
IMMEDIATE SOURCE:  
CLONE: 92-2  
FEATURES:  
FEATURE KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic  
OTHER INFORMATION: storage protein  
OTHER INFORMATION: /product= "protein"  
OTHER INFORMATION: /gene= "ssp"  
OTHER INFORMATION: /standard\_name= "5.11.11.5"  
OTHER INFORMATION: "5.11.11.5"  
US-08-474-633A-63

Query Match 0.54; Score 24; DB 1; Length 97;  
Best Local Similarity 58.3%; Pred. No. 2.2e+03;  
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 1120 gattatgaggtgattacacagaggaattacaggaattggaagtagtagtagtagtag 1179  
DB 10 GAGATGAGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 69  
Qy 1180 agtgaagagaa 1191  
DB 70 AGAGAGATGAA 81

RESULT 14  
PCT-US92-06412-54  
Sequence 54, Application PCT/US9206412  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA: 07/243,006  
FILING DATE: 9 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda Aramethy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DHS alpha  
IMMEDIATE SOURCE:  
CLONE: 92-2  
FEATURES:  
FEATURE KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic storage protein  
OTHER INFORMATION: /product= "protein"  
OTHER INFORMATION: /gene= "ssp"  
OTHER INFORMATION: /standard\_name= "5.11.11.5"  
PCT-US92-06412-54

Query Match 0.54; Score 24; DB 5; Length 97;  
Best Local Similarity 58.3%; Pred. No. 2.2e+03;  
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 1120 gattatgaggtgattacacagaggaattacaggaattggaagtagtagtagtagtag 1179  
DB 10 GAGATGAGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 69  
Qy 1180 agtgaagagaa 1191  
DB 70 AGAGAGATGAA 81





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/codon_start=1
/product="protein kinase 4"
/protein_id="AAA33189.1"
/db_xref="GI:167724"
/tranlation="NULLDYGHIKLTDFGFAKRIITENKSMC"

BASE COUNT      36 a   12 c   14 g   25 t
ORIGIN

Query Match      0.6%; Score 29.6; DB 3; Length 87;
Best Local Similarity 59.5%; Pred. No. 1.8e+04;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 4051 aaatcttccttaccctctggttaatacaactgggagattttggtgttcagtaag 4110
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 AATCTAATTAATGATCATATGATGACATATTAAGCTCACAGATTTTGGATTGCGAAMAGA 60

Qy 4111 ctcaaaaacaatgccagaccatg 4134
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 61 ATCACAGACATACCAAGATG 84

RESULT 2
AR007403/c
LOCUS      AR007403      100 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5750497.
ACCESSION  AR007403
VERSION     AR007403.1 GI:3966887
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 100)
AUTHORS   Havelund S., Halstr. o slashed m.J., Jonassen I., Andersen, A. Sloth.
          and Markussen T.
TITLE     Acylated insulin
JOURNAL   Patent: US 5750497-A 4 12-MAY-1998;
          Location/Qualifiers
FEATURES   source
            29 a   22 c   23 g   26 t
            /organism="unknown"

Query Match      0.5%; Score 26; DB 6; Length 100;
Best Local Similarity 55.6%; Pred. No. 1.7e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 4469 aagaatgaagctagtgaatagatggactggaaattcttcttaactactgtatgtaa 4528
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 97 AAGCTGAGAGCGTACGGTATCGTTGACATGTGTACTTCTATCTTCTTTGTAC 38

Qy 4529 tattacataaagactgtgtgagaagcag 4558
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 37 CAATTGGAAAAGTACTGTGCTTAGACGCAG 8

RESULT 3
AF025984
LOCUS      AF025984      96 bp      DNA      linear      VMT 30-OCT-1997
DEFINITION Paralicthys dentatus lactate dehydrogenase (LDHA) gene, allele
            PdLDHA2, Intron 6.
ACCESSION  AF025984
VERSION     AF025984.1 GI:2570847
KEYWORDS   summer flounder.
SOURCE     Paralicthys dentatus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
          Pleuronectoidae; Paralicthidae; Paralicthys.
REFERENCE  1 (bases 1 to 96)
AUTHORS   Quattro, J.M. and Jones, W.J.

TITLE      Amplification Primers That Target Locus-Specific Introns in
JOURNAL    Actinopterygian Fishes
REFERENCE  2 (bases 1 to 96)
AUTHORS    Quattro, J.M. and Jones, W.J.
TITLE      Direct Submission
JOURNAL    Submitted (22-SEP-1997) Biological Sciences, University of South
          Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
FEATURES   Location/Qualifiers
            source
              1..96
              /organism="Paralicthys dentatus"
              /db_xref="taxon:66718"
              1..96
              /gene="LDHA"
              /note="lactate dehydrogenase gene"
              /allele="PdLDHA2"
              1..96
              /gene="LDHA"
              /number=6
            intron
              24 a   22 c   20 g   30 t
            BASE COUNT
            ORIGIN

Query Match      0.5%; Score 25.4; DB 5; Length 96;
Best Local Similarity 64.4%; Pred. No. 2.4e+05;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 4423 gccagccagcclccgaccattctgttgcagggtttgcacagatgaagatgaagcct 4481
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 14 GICGGACAAATCCTAGACGATTCAATTCACAAAACAGCTGTCCACATGATTAATGACTCT 72

RESULT 4
AX033167
LOCUS      AX033167      70 bp      DNA      linear      BCT 21-SEP-2000
DEFINITION Sequence 3 from Patent WO0045176.
ACCESSION  AX033167
VERSION     AX033167.1 GI:10280029
KEYWORDS   Escherichia coli.
SOURCE     Escherichia coli.
ORGANISM   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
          Escherichia.
REFERENCE  1 (bases 1 to 70)
AUTHORS   Gallusser, A., Karl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.
TITLE     Method of identifying n-terminal probnp
JOURNAL   Patent: WO 0045176-A 03-AUG-2000;
          GALLUSSER, ANDREAS (DE); KARL, JOHANN (DE); LILL, HELMUT (DE);
          STAHL, PETER (DE); KRUEGER, KERSTIN (DE); BORGYA, ANNELEISE (DE);
          ROCHE DIAGNOSTICS GMBH (DE)
          Location/Qualifiers
FEATURES   source
            1..70
            /organism="Escherichia coli"
            /db_xref="taxon:562"
            10 a   19 c   21 g   20 t
            BASE COUNT
            ORIGIN

Query Match      0.5%; Score 25.2; DB 1; Length 70;
Best Local Similarity 62.9%; Pred. No. 2.7e+05;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1778 agggcgccctgctatgaagcagctaccagttcatgtgcagagagttcttgagagact 1837
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 8 AGCCAGCTCTGTTCAACCTGCAGTTCGACAGATTACCTCCTGCAGCTGTTACCGCTTTCC 67

Qy 1838 tg 1839
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Db 68 TG 69

RESULT 5
AX033159

```

LOCUS AX033159 70 bp DNA linear PAT 21-SEP-2000  
 DEFINITION Sequence 3 from Patent WO0045176.  
 ACCESSION AX033159  
 VERSION AX033159.1 GI:10280023  
 KEYWORDS  
 SOURCE Escherichia coli.  
 ORGANISM Escherichia coli.  
 Bacteria; Proteobacteria; gamma subdivision, Enterobacteriaceae;  
 Escherichia.  
 1 (bases 1 to 70)  
 REFERENCE Callusari, A., Kari, J., Lill, H., Stahl, P., Krueger, R. and Borgya, A.  
 A method of identifying a terminal probop  
 TITLE PATENTER ANDREA, DE; KARI, JOMAN (DE); LILL, HELMUT (DE);  
 JOURNAL STAND, PETER (DE); KRUEGER, KERSTIN (DE); BORGIA ANNELESE (DE);  
 MEDLINE ROCHE DIAGNOSTICS GSKH (DE)  
 87166013  
 COMPUTE Draft entry and computer-readable sequence for [1] kindly provided  
 by S.H. Chang, 02-FEB-1987.  
 FEATURES  
 source 1..70  
 Location/Qualifiers  
 /organism="Escherichia coli"  
 /db\_xref="taxon:562"  
 BASE COUNT 10 a 19 c 21 g 20 t  
 ORIGIN

Query Match 0.5% Score 25.2; DB 6; Length 70;  
 Best Local Similarity 62.9%; Pred. No. 2.7e+05;  
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 Oy 1778 agggcgctgctgtagagcagctactaccagttcagctcaggggtcttgaggact 1837  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 8 AGGGAGGCTGTTCACCTCGAGTTCGACAGTTTACCTCGAGTTCGAGTTC 67  
 Oy 1838 tg 1839  
 ||  
 Db 68 TG 69

RESULT 6  
 LOCUS 165769 99 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 5 from patent US 5668294.  
 ACCESSION 165769  
 VERSION 165769.1 GI:2482239  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 99)  
 Koehler, R. B. and Summers, A. O.  
 TITLE Metal resistance sequences and transgenic plants  
 JOURNAL Patent: US 5668294-A 5, 16-SEP-1997;  
 FEATURES  
 source 1..99  
 Location/Qualifiers  
 /organism="unknown"  
 BASE COUNT 29 a 21 c 25 g 24 t  
 ORIGIN

Query Match 0.5% Score 25.2; DB 6; Length 99;  
 Best Local Similarity 58.3%; Pred. No. 2.8e+05;  
 Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
 Oy 3026 atgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3085  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2 AAGCCCAAGCTTATAGCTGCTGTACTCTCTGCAITTCGATCGAAGGCATTGAAGTGC 61  
 Oy 3085 ttgattttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3119  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 62 GTGAGACTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 95

RESULT 7  
 RABPFM18

LOCUS RABPFM18 81 bp DNA linear MM 27-APR-1993  
 DEFINITION Rabbit muscle phosphofructokinase gene, exon 18.  
 ACCESSION M14473 J02702  
 VERSION M14473.1 GI:165622  
 KEYWORDS Phosphofructokinase.  
 SEGMENT 18 of 22  
 SOURCE Rabbit (New Zealand) DNA, clone lambda-Charon 4APFK.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 83)  
 Theobald, R., Kach, C., Fracet, B.A., Putney, S.D. and Chang, S.H.  
 TITLE Protein structure, function, and tissue specific  
 JOURNAL J Biol Chem. 262, 4195-4199 (1987)  
 MEDLINE 87166013  
 COMPUTE Draft entry and computer-readable sequence for [1] kindly provided  
 by S.H. Chang, 02-FEB-1987.

FEATURES  
 source 1..83  
 Location/Qualifiers  
 /organism="Oryctolagus cuniculus"  
 /db\_xref="taxon:9986"  
 /note="PFK intron Q"

Intron 16..77  
 exon 78..>83  
 Intron 23 a 13 c 27 g 20 t  
 BASE COUNT About 719 bp after segment 17.  
 ORIGIN

Query Match 0.5% Score 25; DB 4; Length 83;  
 Best Local Similarity 61.5%; Pred. No. 3.1e+05;  
 Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
 Oy 1737 gagtattaaagcagctgtgagagagctgtaagagctctctgagagagcgtctgatgaa 1796  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 18 GAATGTTCAACACTCTGTCGAAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 77  
 Oy 1797 gcaat 1801  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 78 GTACT 82

RESULT 8  
 AX173377/C  
 LOCUS AX173377 92 bp DNA linear PAT 03-JUL-2001  
 DEFINITION Sequence 31 from Patent WO0142445.  
 ACCESSION AX173377  
 VERSION AX173377.1 GI:14598152  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM artificial construct.  
 REFERENCE 1 (bases 1 to 92)  
 Murthy, R.R., Collins, P.L., Schmidt, A.C., Durbin, A.P.,  
 Skladopoulos, M.H. and Tan, T.  
 TITLE Use of recombinant parainfluenza viruses (pivs) as vectors to  
 protect against infection and disease caused by piv and other human  
 pathogens  
 JOURNAL Patent: WO 0142445-A 31 14-JUN-2001;  
 The Secretary of the Department of Health and Human Services (US)  
 FEATURES  
 source 1..92  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Reverse primer for MSV A G gene insert"

BASE COUNT 20 a 12 c 26 g 34 t  
 ORIGIN

Query Match 0.5% Score 24.8; DB 6; Length 92;



```

195107.1 GI:3939577
.
Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 71)
AUTHORS Toothman,P.J., Ringquist,S. and Gold,L.
TITLE High affinity TGF-beta, nucleic acid ligands and inhibitors
JOURNAL Patent: US 5731424-A 78 24-MAR-1998:
FEATURES
    Location/Qualifiers
        1..71
            /organism="unknown"
BASE COUNT 15 a 16 c 22 g 18 t
ORIGIN
Query Match 0.5%; Score 24.6; DB 6; Length 71;
Best Local Similarity 65.5%; Pred. No. 3.9e+05;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 3958 gaacatgtagctggctgtattccaaagcagcaccattggatcgatccctccc 4012
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GAAGACGTAAGTAAGTAGTATTAAACATACCCCGCTGGCGCATCGTCTCC 2

RESULT 12
S76509/c
LOCUS S76509
DEFINITION D158 (A) (hypervariable minisatellite MS32) [human, individual
MACH, Genomic, 73 nt].
ACCESSION S76509
VERSION S76509.1 GI:243382
KEYWORDS
SOURCE human individual MACH.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 73)
AUTHORS Monkton,D.G. and Jeffreys,A.J.
TITLE Minisatellite 'isoallele', discrimination in pseudohomozygotes by
single molecule PCR and variant repeat mapping
JOURNAL Genomics 11 (2), 465-467 (1991)
NEEDLINE 92120671
REMARK GenBank staff at the National Library of Medicine created this
entry [MCBI gibbsq.76509] from the original journal article.
This sequence comes from Figure 2.
FEATURES
    source
        1..73
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
    gene
        1..73
            /gene="D158"
            /allele="A"
BASE COUNT 41 a 0 g 32 t
ORIGIN
Query Match 0.5%; Score 24.4; DB 9; Length 73;
Best Local Similarity 60.6%; Pred. No. 4.5e+05;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 4914 tgtaatgcgaagcgcgattctcgaatttcagaagaaggtcttttttcataaacggt 4973
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 TATTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13

Qy 4974 ttaull 4979
|||||
Db 12 TTTATT 7

RESULT 13
LOCUS DROTRAN51/c
DEFINITION DROTRAN51

```



Result	No.	Query			DB	ID	Description
		Score	Match	Length			
		27	2	0.5	78	18	Mouse p33-recognt
C	1	26	6	0.5	92	12	Human secreted pro
		26	6	0.5	92	12	Human insulin deri
C	4	25	2	0.5	60	22	Human G-protein su
		25	2	0.5	70	21	Human B22a, B22b
C	5	25	2	0.5	70	21	Human g-secretase
		25	2	0.5	89	16	Human AT22086
C	6	25	2	0.5	99	18	Human AT22344
		25	2	0.5	99	18	Human AT22344
C	8	25	2	0.5	99	20	Human AT22894
		25	2	0.5	99	20	Human AT22894
C	9	25	2	0.5	54	21	GFP LentiG15 for









CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;

Query Match 0.5%; Score 25; DB 22; Length 91;  
 Best Local Similarity 61.5%; Pred. No. 5.1e+03;  
 Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 3815 acgattgaaatattcgagagcatcaacaccccaatctggttcggfattlgtgtgg 3874  
 DB 67 AAGAAATTATTATGATGAAGACTGTAAACACCAATAATTGTCATTATTGGAAGCT 8

OY 3875 agctc 3879  
 DB 7 ATCTC 3

RESULT 11  
 AAC12392/C  
 ID AAC12392 standard; cDNA; 77 BP.

XX AAC12392;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 16467.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.

OS Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST) GENSEPT.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX MPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

PS Claim 1; SEQ ID 16467; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNA or poly(A) RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.

XX Sequence 77 BP; 27 A; 14 C; 15 G; 21 T; 0 other;

Query Match 0.5%; Score 24.8; DB 21; Length 77;  
 Best Local Similarity 60.3%; Pred. No. 5.2e+03;  
 Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 301 gactcagtggtggtatcttgcacaaatccattccagatgtggatctcaataagcct 360  
 DB 74 GACTGTGTAGTGTGCTATTGTTTAAATAATTAATACCTCCCATTCCTCTGGGATTAAGTCT 15

OY 351 taccctcag 368  
 DB 14 TATCTCAG 7

RESULT 12  
 AAS06930/C  
 ID AAS06930 standard; DNA; 92 BP.

XX AAS06930;

DT 12-SEP-2001 (first entry)

DE Reverse PCR primer for RSV A G gene insert.

XX Infectious chimeric parainfluenza virus; antigenic determinant;  
 KW nucleocapsid phosphoprotein; large polymerase; attenuated vaccine;  
 KW human PIV1; HPIV1; HPIV2; HPIV3; RSV; pathogen; measles; PCR primer;  
 KW respiratory syncytial virus; respiratory tract infection; bovine; ss.

OS Human respiratory syncytial virus.

PN HQ200142445-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000MO-US33293.

PR 10-DEC-1999; 99US-0170105.

PR 10-DEC-1999; 99US-0458813.

PR 10-DEC-1999; 99US-0459062.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Murphy BR, Collins PL, Schmlidt AC, Durbin AP, Skladopoulos MH;

XX MPI; 2001-356173/37.

XX Isolated infectious chimeric parainfluenza virus (PIV), useful in an  
 PT attenuated vaccine to elicits an immune response against one or more  
 PT virus(es) selected from human PIV1 (HPIV1), HPIV2 and HPIV3 -

PS Example 10; Page 150; 305pp; English.

XX The present sequence for reverse PCR primer for respiratory syncytial  
 CC virus (RSV) A G gene insert is used with the forward PCR primer  
 CC (AAS06929) in the construction of bovine/humanPIV3-RSV chimeric viruses.  
 CC The sequence is described in an invention relating to novel infectious  
 CC chimeric parainfluenza viruses (PIV3). The virus comprises a major  
 CC nucleocapsid protein (N), a nucleocapsid phosphoprotein (P), a large  
 CC polymerase protein (L), and a partial or complete PIV vector background  
 CC genome, or antigenome combined with one or more heterologous gene(s) or  
 CC genome segment(s) encoding one or more antigenic determinants of one or  
 CC more heterologous pathogen(s) to form a chimeric genome or antigenome.  
 CC The chimeric PIV is useful in an attenuated vaccine to elicit an immune  
 CC response against one or more virus(es) selected from human PIV1 (HPIV1),  
 CC HPIV2 and HPIV3. The chimeric PIV may also elicit a polyspecific immune  
 CC response against HPIV3, measles or RSV. An immunospecific composition  
 CC may also contain two chimeric PIVs, where the first chimeric PIV elicits  
 CC an immune response against HPIV3 and the second chimeric PIV elicits an  
 CC immune response against HPIV1 or HPIV2, and where both the first and  
 CC second chimeric PIVs elicit an immune response against the non-PIV  
 CC pathogen. Chimeric HPIV3, HPIV1 and HPIV2 are useful as vaccines to  
 CC prevent measles and upper or lower respiratory tract infections





RESULT 15  
AAT65208/c  
ID AAT65208 standard; DNA: 71 BP.  
XX AC AAT65208;  
XX DT 10-SEP-1997 (first entry)  
XX DE Transforming growth factor beta-1 binding ligand D 11.  
XX KW Transforming growth factor; beta-1; TGF-beta-1; binding ligand;  
XX KW Identification; SELEX; anti-mitogenic; inhibition; cell;  
XX KW Systematic Evolution of Ligands by EXponential enrichment;  
XX KW epithelial; proliferation; diagnosis; treatment; fibroids;  
XX KW kidney; lung; liver; dermal scarring; restenosis; as.  
XX OS Synthetic.  
XX PN W09618579-A1.  
XX PD 05-DEC-1996.  
XX PF 30-MAY-1996; 96WO-US08014.  
XX PR 20-MAR-1996; 96US-0618693.  
XX PR 02-JUN-1995; 95US-0458423.  
XX PR 02-JUN-1995; 95US-0458424.  
XX PR 05-JUN-1995; 95US-0465591.  
XX PR 05-JUN-1995; 95US-0465594.  
XX PR 07-JUN-1995; 95US-0479725.  
XX PR 07-JUN-1995; 95US-0479783.  
XX PA (NEXS-) NEXSTAR PHARM INC.  
XX PI Gold L, Janjic N, Pogratis M, Ringquist S, Toothman RJ;  
XX WPI: 1997-034387/03.  
XX PT Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF  
XX PT using SELEX, used in the diagnosis and treatment of proliferative  
XX PT disorders  
XX PS Claim 15; Page 123; 209pp; English.  
XX CC The present sequence, a transforming growth factor beta-1  
XX CC (TGF-beta-1) binding ligand, was identified by Systematic Evolution  
XX CC of Ligands by Exponential enrichment (SELEX). Briefly a candidate  
XX CC mixture of nucleic acids was contacted with TGF-beta-1, and nucleic  
XX CC acids having an increased affinity to TGF-beta-1 partitioned from  
XX CC the remainder of the mixture. The partitioned nucleic acids were  
XX CC then amplified to yield a mixture of nucleic acids enriched for  
XX CC sequences with higher affinity and specificity for binding to  
XX CC TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit  
XX CC epithelial cell proliferation, or in the diagnosis and treatment of  
XX CC TGF-beta-1 mediated pathological conditions, e.g. fibrotic  
XX CC conditions such as fibroids of the kidney, lung and liver and more  
XX CC acute conditions such as dermal scarring and restenosis.  
XX SQ Sequence 71 BP: 15 A; 16 C; 22 G; 18 T; 0 other;  
  
Query Match 0.5%; Score 24.6; DB 18; Length 71;  
Best Local Similarity 65.5%; Pred. No. 5.7e-03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
  
QY 3958 gacacgtattagcgttcacagacagatccatcgatccagtcctcc 4012  
DB 56 GAGACGTAGTACTAGTATTAAACATACCCGCCCGCCGATGCGTCC 2

Search completed: May 29, 2002, 13:05:25  
Job time: 9833 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:13:38 : Search time 35:8.59 seconds  
(without alignments)  
19141.135 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990

Sequence: - ctgaagactctccagtg.....ggtttatttaggaagc 4990

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 1376207 seqs, 674877542 residues

Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gp\_estl:\*

10: gp\_est2:\*

11: gp\_hic:\*

12: gp\_gss:\*

13: gp\_gss\_hum:\*

14: em\_gss\_inv:\*

15: em\_gss\_pin:\*

16: em\_gss\_vit:\*

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39.8	0.8	95	9	AA990067
2	29	0.6	70	9	AA990364
3	28.6	0.6	71	9	AT767078
4	27.8	0.6	83	10	B063432
5	27.8	0.6	91	10	B132285
6	27.8	0.6	100	9	B132285
7	27.8	0.6	100	9	B132285
8	27.4	0.5	98	9	AT054386
9	27.4	0.5	98	9	AT054386
10	26.8	0.5	100	10	C53110
11	26.6	0.5	81	10	B573242
12	26.6	0.5	82	10	BF101686
13	26.4	0.5	87	9	AA267457
14	26.4	0.5	95	9	AA946634
15	26.4	0.5	95	10	R93104
16	26.2	0.5	78	10	R40354
17	26.2	0.5	93	9	AV551027

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
18	26.2	0.5	93	10	TG2011							
19	26	0.5	78	10	B1858071							
20	26	0.5	85	12	BH127076							
21	26	0.5	88	9	AA665746							
22	26	0.5	99	9	A1251245							
23	25.8	0.5	78	9	A1035450							
24	25.8	0.5	83	9	AA515897							
25	25.8	0.5	91	9	A1340694							
26	25.8	0.5	91	9	A1894107							
27	25.6	0.5	73	9	A1142936							
28	25.6	0.5	85	9	A1086378							
29	25.6	0.5	85	9	AV532477							
30	25.4	0.5	79	9	AA149985							
31	25.4	0.5	93	12	AZ961698							
32	25.4	0.5	91	10	C19910							
33	25.4	0.5	92	12	AF149669							
34	25.4	0.5	93	9	AA669624							
35	25.4	0.5	94	9	AL652095							
36	25.4	0.5	95	9	AA575542							
37	25.4	0.5	99	10	B032479							
38	25.4	0.5	99	10	B032479							
39	25.4	0.5	99	10	B032479							
40	25.4	0.5	99	10	B032479							
41	25.2	0.5	81	9	AA51813							
42	25.2	0.5	86	9	A133913							
43	25.2	0.5	88	10	C01741							
44	25.2	0.5	94	10	B1943018							
45	25.2	0.5	97	12	TA130801P							

## ALIGNMENTS

AA990067 95 bp mRNA linear EST 02-JUN-1998  
us58102.r1 Soares-Thymus\_2NDMT Mus musculus cDNA clone  
IMAGE:1361691.5', mRNA sequence.  
AA990067  
AA990067.1 GI:3173431  
EST.

Mus musculus  
Eukaryota: Mammalia: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
(bases 1-95)  
Garratt, R., Hillier, L., A'Hearn, M., Bowles, M., Dietrich, M., Dubuque, T.,  
Garratt, R., Hillier, L., A'Hearn, M., Bowles, M., Dietrich, M., Dubuque, T.,  
Schallerberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterson, R.  
The WashU-HMNI Mouse EST Project  
Unpublished (1996)  
Contact: Maira M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 285 1800  
Fax: 314 285 1810  
Email: mhmm@wustl.edu  
This clone is available royalty-free through LNCX: contact the  
IMAGE Consortium (info@imgc.lncl.gov) for further information.  
Seq primer: -28m3 rev2 EST from Amersham  
High quality sequence scop: 82.  
Location/Qualifiers:  
1  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1361691"  
/clone\_lib="Soares\_Thymus\_2NDMT"  
/sex="male"

AA990067 95 bp mRNA linear EST 02-JUN-1998  
us58102.r1 Soares-Thymus\_2NDMT Mus musculus cDNA clone  
IMAGE:1361691.5', mRNA sequence.  
AA990067  
AA990067.1 GI:3173431  
EST.

Sites 2, Eco RI. Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2bH9, pregnant uterus NBH9, and fetal heart NBH19) were mixed and 55 circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260332-265233, 340488-345479, and 484488-489479.

```
Query Match      0.68; Score 29; DB 9; Length 70;
Best Local Similarity 71.7%; Pred. NO. 1.4e+04;
Matches 38; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
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SOURCE: human.  
 ORGANISM: Homo sapiens  
 Eukaryota; Chordata: Vertebrate: Euteleostomi:  
 Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Homo.  
 1. (bases 1 to 71)  
 NC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Straube, Ph.D.

```

FEATURES
  source
    High quality sequence stop: 70.
    Location/Qualifiers
      1..71
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_image="IMAGE:2400828"
        /clone_lib="NCI_CGAP_Kid12"
        /tissue_type="2 pooled tumors (clear cell type)"
        /lab_host="DH10b"
        /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
p.asn1d DNA from the normalised library NCI_CGAP_Kid5 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(CloneIDs 132912-132931, 147168-147290) and
1492104-149325)."
        /subtraction="Subtraction by Bento Soares and M.
Fatima Bonaldo."
      22 a 16 c 7 g 26 t

```



Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, H.,  
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,  
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,  
Shio, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and  
Wilson, R.

The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James  
McCarter (chiapell@wustl.edu & jmcarter@wustl.edu) at  
Washington University, St. Louis. DNA Sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
putative full length read

The vector to vector length is 95

Seq primer: -40RP from Glbco.

Location/Qualifiers

1. 94

/organism="Parastromyloides trichosuri"

/db\_xref="taxon:131310"

/clone\_lib="Parastromyloides trichosuri FL pAMP1 v1"

Chiapelli McCarter"

/dev\_stage="Free Living"

/lab\_host="DH10B"

/note="vector: pAMP1 (Gibco); Site\_1: NotI; Site\_2: SalI;

The library was constructed by Brandi Chiapelli and Dr.

James McCarter at Washington University, St. Louis. The

cDNA was made by using Dynabead oligo-dT priming (Dynal).

PCR based library using a modified protocol from the

SMART PCR cDNA Synthesis Kit from Clontech. Directionally

cloned into the UDG sites of pAMP1. Nematodes were

provided by Dr. Warwick Grant of AgResearch, New Zealand

(warwick.grant@agresearch.co.nz)."

42 a 9 c 12 g 31 t

BASE COUNT  
ORIGIN

Query Match 0.68; Score 27.8; DB 10; Length 94;

Best Local Similarity 62.0%; Pred. No. 3.1e+04;

Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 3542 agagtcgctcgattgtttgagaaagaggtaccgagaaatgagagaaagagaaatca 3601

|||||

Db 8 AATATGATCCACTGATGAAATTAAGACATCAAAAAGAGGGTGTGTAATATATT 67

|||||

Qy 3602 ttggctcaagtt 3612

|||||

Db 68 TTTATCAAGTT 78

RESULT 7  
LOCUS

AA154655 100 bp mRNA linear EST 19-FEB-1997

mq61c08.r1 Soares\_thymus\_2NBMT Mus musculus cDNA clone IMAGE:583214

5' similar to SM:KCC4\_MOUSE P08414 CALCIUM/CALMODULIN-DEPENDENT

PROTEIN KINASE TYPE IV CATALYTIC CHAIN 1; mRNA sequence.

AA154655

AA154655.1 GI:1726483

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 100)

Marra, M., Miller, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

TITLE  
JOURNAL  
COMMENT

Waterston, R.  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:357862

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: 28M13 rev2 from AmerSham

High quality sequence stop: 1.

Localion/Qualifiers

SOURCE

1. 100

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_lib="IMAGE:583214"

/sex="male"

/tissue\_type="Thymus"

/dev\_stage="4 weeks"

/lab\_host="DH10B"

/note="vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTACCAACTCAAGTGGGAGCGCGGTTTCTTTTCTTTTCTTTTCTTTTCTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p773 vector. RNA

provided by Dr. Bertrand Jordan. Library went through two

rounds of normalization, and was constructed by Bento

Soares and M. Fatima Bonaldo."

24 a 11 c 20 g 45 t

BASE COUNT  
ORIGIN

Query Match 0.68; Score 27.8; DB 9; Length 100;

Best Local Similarity 57.5%; Pred. No. 3.2e+04;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 3977 atlcaagcagatccaccattcgatcaactctctcattgagcatgctccaccctg 4036

|||||

Db 87 ATCAAGCAGCATTTAGAGCATTTAGTACTTACTGACATTAATAATCATCCACCG 28

|||||

Qy 4037 acattaaagrgccaatatcttctcta 4053

|||||

Db 27 ATCTAAAAGCTAGCAATATTCTCTATA 1

RESULT 8  
LOCUS

T85845 91 bp mRNA linear EST 17-MAR-1995

ydb1010.r1 Soares fetal liver spleen rnlfls Homo sapiens cDNA clone

IMAGE:112723 5' similar to gb:X56468.rnal 14-3-3 PROTEIN THETA

(HUMAN); mRNA sequence.

T85845

T85845.1 GI:714197

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 91)

Miller, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M., Holman

M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Morris, J.,

Rifkin, L., Roling, T., Soares, M., Tan, F., Trevisan, E., Waterston

R., Williamson, A., Wohlmann, P. and Wilson, R.

REFERENCE  
AUTHORS



DB 66 TAAA 7C

RESULT 12

## REFERENCE

BASE COUNT

RESULT 13

REF ID: A66001

**SOURCE**

Db 66 TTA 7C

## KEYWORDS

COMMENT

## FEATURES

**NOTES**

322





Email: M-Saber@FRCU.EUN.EG

Seq primer: 8k.

## FEATURES

## Source

**Location/Qualifiers**

2.95

/organism="Schistosoma mansoni"

“strain-“Egyptian”

/db xref="taxon:6183"

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/clone - "SMTBADAMS0038SK"
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/clone_11b="S. mansoni cDNA"
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/cclone_lib="S. mansoni CDNA"
/lab host="E. coli XL Blue"

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/lab_host="E. coli XL blue"
/note="vector: pBluescript II SK+; site_1: EcoRI; site_2:
```

/note=Vector: pBluescript II SK+; site\_1: ECORI; site\_2:  
 loxph: was purified from adult colonies of S. mansoni.  
 mangan

cdna was constructed and cloned simultaneously using

cdDNA was constructed and cloned simultaneously using the pMuescript II SK+ vector. cdNA

vector priming with the pBluescript II SK+ vector. cDNA

was directionally synthesized

vector to the Xhol site." 39 +  
15 0 15 0

15 c 10 g 39 t

31 a

25 C

39 t

39 t

BASE CO  
ORIGIN

BASE CO  
ORIGIN

Query Match 0.58; Score 26.4; DB 10; Length 95;

Query Match 0.30; Score 26.4; DB IO; Best Local Similarity 59.20; Pred. No. 7.3e+04;

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BEST LOCAL SIMILARITY  59.2%;  PRED. NO.: 7.3E+04;
MATCHES  45;  Conservative  0;  Mismatches  31;  Indels  0;  Gaps  0;

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QY 641 acttctttlatacagcccgtaagccatccccgatatattantgaatacttactt /00

DB 3 ACTATGATTATTATAACACTA

Qv 701 tcabaaotcgaactatga 716

QY 701 tcaagtcgactatgg 716

65 TGAAATTTCACCATAG 80



Db 97 AAGTTCAGACGCTAAGGGTATCGTGAACAATGTGTGACTTCTATCTCTCTGTGAC 38

Qy 4529 tattacataaagactgctgctgagaagcag 4528

Db 37 CAATGGAAACTACTGCTCTAGACGCG 8

## RESULT 2

US-08-975-365-4/C

; Sequence 4, Application US/08973365

; Patent No. 6011007

## GENERAL INFORMATION:

APPLICANT: Havelund, Svend

APPLICANT: Halstrom, John

APPLICANT: Jonassen, Ib

APPLICANT: Andersen, Aaser sloth

APPLICANT: Markussen, Jan

TITLE OF INVENTION: ACYLATED INSULIN

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,365

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/400,256

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3985,220-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 100 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-975-365-4

## Query Match

Best Local Similarity 0.5%; Score 26; DB 3; Length 100;

Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 4469 aagaatgaagcctagatgacttggaataatccttaactactactactgtatgtaa 4528

Db 97 AAGTTCAGACGCTAAGGGTATCGTGAACAATGTGTGACTTCTATCTCTGTGAC 38

Qy 4529 tattacataaagactgctgctgagaagcag 4528

Db 37 CAATGGAAACTACTGCTCTAGACGCG 8

## RESULT 3

US-08-427-097-5

; Sequence 5, Application US/08427097

; Patent No. 5668294

## GENERAL INFORMATION:

APPLICANT: Meagher, Richard B.

APPLICANT: Sommers, Anne O.

TITLE OF INVENTION: Metal Resistance Sequences and

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/427,097

FILING DATE: 21-APR-1995

CLASSIFICATION: 80Q

ATTORNEY/AGENT INFORMATION:

NAME: Feiber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 4C-94

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: /desc = "Oligonucleotide"

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-427-097-5

## Query Match

Best Local Similarity 0.5%; Score 25.2; DB 1; Length 99;

Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 3026 atgtctgactaaatgtgagagtgtgaggtacagaccacccaggtggtgagctcaaggt 3085

Db 2 AAGACCAGCTAGGTGAGGTGTTACTGCTGCA7TTTCATGGAAGGCATTGAAGTGC 61

Qy 3086 ttgattttctacaagcaattgaacctgccttat 3119

Db 62 GTGAGCATACTCAGCAAGCCAGTTCCTATAT 95

## RESULT 4

US-08-878-957-5

; Sequence 5, Application US/08878957

; Patent No. 5965796

## GENERAL INFORMATION:

APPLICANT: Meagher, Richard B.

APPLICANT: Summers, Anne O.

APPLICANT: Rugh, Clayton L.

TITLE OF INVENTION: Metal Resistance Sequences and

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release 11.0, Version 11.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,957  
FILING DATE: 19-JUN-1997  
CLASSIFICATION: 800  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/427,097  
FILING DATE: 21-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 3,878  
REFERENCE/DOCKET NUMBER: 40-94A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 base pairs  
TYPE: nucleic acid  
TOPOLOGY: single  
MOLCULE TYPE: other nucleic acid  
HYPOTHETICAL: /desc - "oligonucleotide"  
ANTI-SENSE: NO  
CS-08-878-557-5

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Query Match      0.5%  Score 25.21  DB 2:  Length 99:
Best Local Similarity 54.3%  Pred. No. 1u-03:
Matches 51:  Conservative 0:  Mismatches 43:  Indels 0:  Gaps 0:

3026 atctctcactcaaatgtatgagtgtatgaggtacacacccagglygagctcaggat 3085
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dbb 2  agtaccagctatgataagcctgtttactctgcttccatcgatgagcattcagctoc 61
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

3086 ttattttcttcacacactcagcctctcttat 3119
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
dy 62 gtgagcattactcaagcaagcgaactgttcctatat 95
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RESULT 5  
US-08-458-423A-78/C  
Sequence 78, Application US/08458423A  
Patent No. 5731144  
GENERAL INFORMATION:  
APPLICANT: PENELOPE J. TOOTHMAN  
APPLICANT: STEVEN RINGOICST  
APPLICANT: LARRY GOLD  
TITLE OF INVENTION: HIGH AFFINITY TGFA INHIBITORS  
TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESS: Swanson and Bratschan, L.L.C.  
STREET: 8400 East Prentice Avenue, Suite #200  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
CONSUMER READABLE FORM:  
COMPACT RIFLEX Discette, 3.5 inch, 1.44 Mb storage  
COMPUTER SYSTEMS COMPANY  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wardperfect 3.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458.423A  
FILING DATE: 2-JUNE-1995  
CLASSIFICATION: 536

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 07/74.131
3 FILING DATE: 10-JUNE-1991
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 07/536.428
6 FILING DATE: 11-JUNE-1990
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 07/964.524
9 FILING DATE: 21-OCTOBER-1992
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 06/117.991
12 FILING DATE: 8-SEPTEMBER-1993
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 07/931.473
15 FILING DATE: 17-AUGUST-1992
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Diane H. McClearn
18 REGISTRATION NUMBER: 31,950
19 REFERENCE/DOCKET NUMBER: NEX 34.1
20 TELEPHONE: (103) 703,3333
21 TELEPHONE: (103) 703,3333
22 INFORMATION FOR SFO TO NO: 78:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 71 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: DNA
29 US-08-458-423A-78
30
31 Query Match: 0.5% Score 24.6; DB 1; Length 71;
32 Best Local Similarity 65.5%; Pred. No. 1.2e+03;
33 Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
34
35 Qy 3958 gacacatgatcagctcgtatcagacatcattgcacacagctccac 4012
36 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
37 DB 56 GAGACGCTAGTAAGTAGTATTAAAAACAATACCCGCCCTGGCCGCTCCTCC 2
38
39 RESULT 6
40 US-08-458-424B-78/c
41 Sequence 78; Application US/08458424B
42 Patent No. 5731424
43 GENERAL INFORMATION:
44 APPLICANT: GEORGE J. TOOTHMAN
45 APPLICANT: STEVEN RINGQUIST
46 APPLICANT: LARRY GOLD
47 TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
48 TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
49 NUMBER OF SEQUENCES: 89
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: Swanson and Bratschan, L.L.C.
52 STREET: 8400 East Pleasant Avenue, Suite #200
53 CITY: Denver
54 STATE: Colorado
55 COUNTRY: USA
56 ZIP: 80111
57
58 COMPUTER READABLE FORM:
59 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
60 COMPUTER: IBM compatible
61 OPERATING SYSTEM: MS-DOS
62 SOFTWARE: WordPerfect 5.1
63 CURRENT APPLICATION DATA:
64 APPLICATION NUMBER: US/08/458,424B
65 FILING DATE: 2-JUNE-1995
66 CLASSIFICATION: 356
67 PRIOR APPLICATION DATA:
68 APPLICATION NUMBER: 07/74.131
69 FILING DATE: 10-JUNE-1991
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: 07/536.428

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;; FILING DATE: 11-JUNE-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/964,624  
;; FILING DATE: 21-OCTOBER-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/117,993  
;; FILING DATE: 8-SEPTEMBER-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/931,473  
;; FILING DATE: 17-AUGUST-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Diane B. McClearn  
;; REGISTRATION NUMBER: 33,960  
;; REFERENCE/DOCKET NUMBER: NEX 34-2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (303) 793-3333  
;; TELEFAX: (303) 793-3433  
;; INFORMATION FOR SEQ ID NO: 78:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 71 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-458-424B-78  
Query Match 0.58; Score 24.6; DB 1; Length 71;  
Best Local Similarity 65.58; Pred. No. 1.2e+03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
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Db 56 GAGACGCTAGCTAGTACTATTAAACATACCCCTGGCCGCGATCGTCTCC 2  
RESULT 7  
US-08-973-124-78/c  
; Sequence 78, Application US/08973124  
; Patent No. 6207816  
; GENERAL INFORMATION:  
; APPLICANT: LARRY GOLD et al.  
; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
; TITLE OF INVENTION: LIGANDS TO GROWTH  
; TITLE OF INVENTION: FACTORS  
; NUMBER OF SEQUENCES: 304  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/08014  
; FILING DATE: 30-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/458,423  
; FILING DATE: 02-JUNE-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/458,424  
; FILING DATE: 02-JUNE-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,594

;; FILING DATE: 05-JUNE-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/465,591  
;; FILING DATE: 05-JUNE-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/479,725  
;; FILING DATE: 07-JUNE-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/479,783  
;; FILING DATE: 07-JUNE-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/618,693  
;; FILING DATE: 20-MARCH-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Barry J. Swanson  
;; REGISTRATION NUMBER: 33,215  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (303) 793-3333  
;; TELEFAX: (303) 793-3433  
;; INFORMATION FOR SEQ ID NO: 78:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 71 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-973-124-78  
Query Match 0.58; Score 24.6; DB 4; Length 71;  
Best Local Similarity 65.58; Pred. No. 1.2e+03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Oy 3958 gaacatgtgattagctgtattcaagacagatcacccattggatcaacgctctcc 4012  
Db 56 GAGACGCTAGCTAGTACTATTAAACATACCCCTGGCCGCGATCGTCTCC 2  
RESULT 8  
PCT-US96-08014-78/c  
; Sequence 78, Application PC/TUS9608014  
; GENERAL INFORMATION:  
; APPLICANT: LARRY GOLD; NEROLJA JANJIC; STEVEN RINGQUIST; NIKOS  
; APPLICANT: PAGRATIS; FENELPE J. TOOTHMAN  
; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
; TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED  
; TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN  
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR (hKGF)  
; NUMBER OF SEQUENCES: 304  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/08014  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/458,423  
; FILING DATE: 02-JUNE-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/458,424  
; FILING DATE: 02-JUNE-1995









```

RESULT 15
US-08-672-158A-8
; Sequence 8: Application US/08672158A
; Patent No. 5770371
; GENERAL INFORMATION:
; APPLICANT: Sheryl Thompson
; TITLE OF INVENTION: Modification of Cryptic Splice Sites In
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5770371c No. 5770371dsk of No. 5770371th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672.158A
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4855,000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-672-158A-8

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Query Match 0.58; Score 23.8; DB 1; Length 83;
Best Local Similarity 72.18; Pred. No. 2.3e+03;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1352 gtatgacattgtctgactctattattatagaccatttctagacaa 1394
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DB 17 GTAGACGTATGTGAGTATAGTGTGCTACTCCATCTGTGCCAA 59

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Search completed: May 29, 2002, 12:56:56  
Job time: 9665 sec